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CLOYVDNKGFPTWI.KLDKKVSAQEVRKESPLQFKFPAKFYPEDVAEELIQDITGKLF
FLQVKEGILSDEIXCPPETAYLLGSYRVQAKFGDVKELHKAGYLGSERLIDORYMDG
HKLTRIDOWEDH IQVWHAEHERMI.KDSAMI.FYI.KIADDIEMYGINFEIKNKGTTDIMI.
GVDALGINIYEKDDKLITPKIGFPWSEIRNISFNDKKFVIKPIDKKADDFVFYAPHIRI
                      MAM 11-JUN-1993
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PREBOWHFEKFELMFLGYPEKTFRAKELSPOLGARLKLEFEKKAGERGLFAD
RLAALKPETERGAADGTKSGEGLATELAEYTATALLEEPRRKENVBENGLRAK
FAALKPETERGAADGTKSGEGLATELAEYTATALLEEPRRKENFYBENGLRAK
FAQUOLLVKTREELHAWATAPPPFVEVVLYNTIVHEGSPGEGTELSAELSSEGTLLDDRN
FEKR TTFARKNERVOROLMTLTSELSGARDENKRTHNDTTHNENMRGGRDKYKTLROT
RGGRV TFARKNERVOROLMTLTSELSGARDENKRTHNDTTHNENMRGGRDKYKTLROT
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                                                                                                                                                    Eukaryoia; Melazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaila; Eutheria; Cetarliodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
1 (bases 1 to 2514)
Horgson.C.M.; Zhao,H.; Sajjoh,K.; Duman,R.S. and Nestler,E.J.
Ezrin and ostconcetin, two proteins associated with ceil shape and growth, are entiched in the long coeruleus
Mol. Cell. Neurosci. 4, 64-73 (1993)
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Turunen,O., Wingvist,R., Pakkanen,R., Grzeschik,K.H., Wahlstrom,T.
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Human placenta, cDNA to mKNA.
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J05021
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Conservative:
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/db_xref="G1:289408"
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/organism-"Hos taurus"
/db_xrcf-"taxon:9913"
/lissue_Lype-"brain"
152. .1897
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Draft entry and computer-readable sequence for [1] kindly submitted by O.Turunen, 31-AUG-1989, Location/Qualifiers
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Ab_xxet="61:3402.1"
Ab_xret="GD8:00-120-489"
/!ranslation="MDAELEFAIQPNTTGKQLFF@VVKTIGLREVWYFGLHYVDNKGF
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ELMLRLQDYEEKTKKAERELSEQIQRAIQLEFERKRAGEEABRLEADHMAALRAKEEL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon.9466"
/note="EMBL/GenBank Accession No. X51521"
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GVDALGLINTYEKDDKLTPKTGFPWEREINISTENNFKTVIKTPUTKRITKENPENPYARELPT

GVDALGLINTYEKDDKLTPKTGFPWEREINISTENSTENFKTFUTKTFUTKENFKENENPELPT

REKEGMMREKEELMIKUJUI EEKI KNABRELISTUJULEERKKREDELET KREETU

FRAGMMREKEELMIKUJULEERI KNABRELARTA ALLIETARRKREDEVERMUHRAL

FRAGDDILVKTKEELHIVATTAPPPPPPTYYEDVSYHVÖESIGDIRGEPROTGYSARGESSEGI

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FRAGDDILVKTKEELHIVATTAPPPPTYYEDVSYHVÖESIGDIRGESSEGI
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2 (bases 1 to 3044)
6 Could.K.L., Bretscher.A., Esch.F.S. and Hunter,T.
cDNA cloning and sequencing of the protein tyrosine kinase substrate, czrin, reveals homology to band 4.1
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/db_xre1-"GI:31283"
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/note="czrin (AA 1-586)"
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information about the clone and the sequencing project is available
at http://www.mips.biochem.mpq.de/proj/cDNA/.
                      linear PAL 28-JUN 2002
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Lodes,M.J., Algate,F.A., Fring,S.P., Mannion,J., Renson,D.P. and
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/db_xref="taxon:9606"
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MPKPINVRVTTMDAELEFALQPNTTGKQLFDQVVKTIGLREVWFFGLHYVDNKGFPTW
KLDKFVSAGEVPFERRLQFFFAKRFYPFFVAFAELTQLTZAKLFZCVFKGSLLSDETY
CPPFFAVLLGSYAVGAFFGIVFVFFKSTVT SSFFI I PQVMIGHRITFDQMFDFLOV
WHAEHRGMLKDNAMLEYLKIAQDLEMYGINYFFIKNKGITDLWLGVNALGIN FFRD
                                                                                                                                                                                                                                                                                                                                                                /translation-"GPVGGPVGAAGSTPSTAGAGLGQPLPCGTVVFSGIEDTHQKPK
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YMRRRKPDT I EVQQMKAQAREEKIQKQLERQQLETEKKRRETVEREKEQIMMREKEELM
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AVDQ1KSQEQLAAFLAEYTAKTALLEFARPRKEDEVEEWQHFAKEAQDDLVKTKEELH
LVMTAPPPPPPVYEPVSYHVQESLQDEGAEPTGYSAELSSEG1KDJRNEEKR1TFAK
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                                   /map="6q22-q27"
/clone="DXFZp762H57"
/tissue type="melanoma (MeWo cell line)"
/clone=llb="756" (synosym: hmel2). Vector pSportl, host
/dev_staqe="adult"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo,
1 (bases 1 to 3173)
Strausberg, R.
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                                                                                                                                                                                                                                                                                               /product="Nypothetical protein"
/protein_id="CAB82418.1"
/db_vrof="G1:7*28175"
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/orqanism-"Homo sapiens"
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                    /db_xret-"taxon:9606"
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Query Match:
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Clone distribution: MGC clone distribution information can be found
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FLOVKEGTLSDELYCPPETAVLLIGSYAVQAKFGDYNKEVHKSGYLSSEKLI PORVMDO
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REKROMMREKEFILMI.RLODYEFYTKKAFPET SEGIOPALQLEEFPRPAPAGESAEPILEAD
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RDDRNEEKRITEAFKNERVQRQLLTLSSFLSQARDFNKRTHNDTTHNENMRGGRDKYK
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Human DNA sequence from clone PPI1-507610 on chromosome 6425.2 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /t.ranslation-"MPKPINVRVTTMDAELEFAIQPNTTGKQLFDQVVKTIGLREVWY
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                                                                                                                                                                                     through the I.M.A.G E Consentiam/LLNL at hite//image.llnl.gov
Series: HAAL Plate: 2 Row: a Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9257254.
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan*systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
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Eskar<u>r</u>eta, Metasca; Cherdata; Craniata, Vertebrata; Enfeleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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On Sep 12, 2001 this sequence version replaced qi:14586238.
During sequence assembly data is compared from overlapping clones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"Similar to villin 2 (ezrin)"
                                                                                                                                                                                                                                                                                                                                            /Ordanism_Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:1584 IMAGE:2959:899"
/tissue_type="Coldu, adenocarcinoma"
/lab_bost="DHIOB-R"
                                                                                                          Greene, Mark Ketteman and Anuradha Madan
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/db_xref-"GI:15530243"
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AL589931 ACC23785
AL589931.14 GI:15591370
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                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality as 00); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one ML3 subclone; and the assembly was confirmed by restriction digner. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMHL: SW:, database can be found at.
                       together with a note of the overlapping clone name. Note that the variation annotation may not be tound in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear PRI 19-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ll-507010 is from the library RPCI-11 2 constructed by the group
Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156422. .156454 // Anote-"Sequence from uni-directional primer reads only."
                                                                                                                                                                                                                                                                                                                                                                                       http://www-sanger ac.uk/Projects/~petans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is the entire insert of clone RPI1-507C10 The true right end of olone PPI1-114ML is at 47323 in this sequence. Localion/Qualitiers
1. 215705
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Where differences are found these are annotated as variations
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/clone_lib="FPGI-11.2"
37002, .37057
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A gene family consisting of earin, radixin and mossin. Its specific localization at actin filament/plasma membrane association sites 93055012
                                                                                                                                                                                                                                                                                                                                                                                                  /translation="TGMYGINYFEIKNKKGIDLWLGVDALGLNIYEKDDKLAPKIGFP
                                                                                                                                                                                                                                                                                                                                                                                                                       WSETRNISFNDKKFVIKFIDKKAPDEVFYAFRUFTNKFILQLOM:HHFLYMPPRKDT
IEVQQMKAQAREEKXQNQLERQQLETEKKPPEXVEPEKFQMMPEKEELMLRLQDYED"
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                2. (bases 1 to 478)
Fadiel,A., Chen,Z.C. and Naftolin,F.
Direct Submission
Submittled (2%-SEF-1999) GB/GYM, Yale University, 333 Cedar Street,
New Haven, C: 06520, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Motazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia: Eutheria, Rodentia, Sciurognathi, Muzidae, Murinaa: Mus.
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Sato, N., Fundyama, N., Naqafuchi, A., Yomemura, S., Isakita, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Funaγama,N., Nagafuchi,A., Sato,N., Isukita,S. and Isukita,S. Radixin is a novel member of the band 4.1 family J. Cell Biol. 115 (4), 1039-1048 (1991)
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Submitted (12-701-1991) N. Funayama, National Inst. for
Physiciogram Series, Mysdibli Okaraki 14, JAPAN
2 Chases I to 2701)
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/ceil_line-"Hu&0"
cell_type="leukemia cells"
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/note-"villin 2; kinase substrate"
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Mismatches:
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/db_xref="G1:6063147"
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                                                                                                                                                             /organism-"Homo sapiens"
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/chromosome-"6"
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Alignment Scores
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ERADALWAKEELIRQAQDQIKSGEQLAABLARYTAKIALLEERRRKEGEVERWÜRAK
EQDOLWKTKEELILUWTAPPPPPPPYEPVYIVUGGLODGAEPMGYSAELSSEGT
LDORNERRTTPARTRYAGALGULTLSNELSQAPPENKPTHINDITHNENMEGGEPKYY
TILKOTROGNIKQKIDEFEAM"
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FLQVKD3TLSGETYCPPETAVLA3SYAVQAKF9PYNKEMHKSAYLSSFPLTDQFYNKLY
HKLSPQQWEDPTQVWHAEHPGMLKDSAMLEYLKTAQDFENYATINYEETKNKKGTDLWL
                                                                                                                                                                                                   Zdb_xref="SWISS_PROF:P26040"
Ztranslation="MRKPINVEVIIMOAR: PPAIGPNFTCRGLETGVVKTIGLREVWY
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Mus musculus chromosome 16 clone PP23-3512, WORKING SPAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                     GVDALGENTYERFEREITETER FOR FOR FOR SENDKKEVERPERKARPPEVEY ALKERT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Bodentia, Sciatograthi, Muzidae; Muzinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conscious quality: 124780 bases at least 240
Conscious quality: 150886 bases at least 030
Consensus quality: 159781 bases at least 020
Estimated insert size: 200400; agarcse-up estimation
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/protein_id-"CAA44086.1"
/db_xret-"GI:50881"
/db_xrel="taxon.10090"
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
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Estimated insert size: 180802; sum-of-configs estimation quality coverage: 3.02 in Q20 bases; agarose-tp estimation Quality coverage: 3.34 in Q20 bases; sum-of-configs estimation. A NOTE: Phis is a 'working draft' sequence. It currently a consists of 26 configs. The true order of the pieces is is not known and their order in this sequence record is
                                                                                                                             * as soon as it is available and the accession number will be preserved.
                                                                                       * arbitrary. Gaps between the contids are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence
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contig of 41175 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14 EEC 2001) Harvard Fartners Center for Genetics and Genomics, Harvard Medical School, 65 Landsdowne St., Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                         Han, J., Montgomery, K.T., Crills, G., Loc, E., Long, J., Pomerantz, R., Crishikhes, J.P., Shim, C., Prockey, J., Phomas, P., Portera, A., Gordon, M., Coller, J. S., and Kurberlapati, P., Burtz, J. S., and Kurberlapati, P., Hidh, Throughput. Mouse Sequencing
                                                                                                                                                                                                                                                                                                                  Eukaryota, Metadoa, Chordata, Craniata, Verbebrata, Eutoloostomi,
Mammalia: Eutheria: Rodentia: Sciuroquathi; Muridae; Murirae; Mus
1 (bases 1 to 207782)
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Ioshikhes,I.P and Kucherlapati,R.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (28-JUL-2000) Department of Molecular Genetics, Albert
Einstein College of Medicine Genome Center, 1300 Morris Park Ave
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On Oct 20, 2000 this sequence version replaced gl.10799310.
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Submitted (01 FEB 2000) Department of Molecular Genetics, Albert
Einstein College of Medicine Genome Center, 1900 Morris Park Ave.,
Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                              quality coverage. against EF - N/A quality coverage: 8.5 x in Q20 bases; sum of-configs estimation
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                                                            On Jan 4, 2002 this sequence version replaced qi:11094413.
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216675: contig of 855 bp in length
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217917: contiq of 1222 bp in l
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Chemistry: Dye terminator Bid Dye, 100%
Consensus quality: 212564 at least Q20
*Consensus quality: 211720 at least Q40
*Consensus quality: 210730 at least Q40
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                                                                                               Harvard Partners Genome Center
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/strain="C57BL6/J"
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Montgomery K T - Grills G , Han, L , Lee, P , Leng, L , Pomeranta, P ,
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Montgomery, K.T., Grills, G., Han, J., Lee, E., Long, J., Pemerantz, E.,
Gordon, M., Golls, J.S. and Kucherlapati, R.
Direct, Submission.
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29570: contig of 1837 bp in length
295727: qap of unknown length
297782: contig of 2055 bp in length.
contig of 2715 bp in length gap of unknown length contig of 1443 bp in length
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gap of unknown length
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Parkway, St. Louis, MO 63108, 08A
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Mammalia: Euthoria: Kodentia: Sciurognathi; Muridae; Murinae; Mus.
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                                                             /note-"assembly_name:Contig204"
215752. 215800
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215921 .216675
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//noic_assembly_name:Con!;1202"
216096, .217917
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linear PRI 19-0CT-1999
* is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * tans of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as seen as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                     160757: contig of 56889 bp in length
160857: gap of unknown length
284417: contig of 123560 bp in length
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285468: gap of unknown length
286508: contig of 1040 bp in length.
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1604. 4585
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/noter-massembly_name:Contig103"
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160858. 284417
/coro-"assembly_name:Contigl06"
284518. 285368
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/-br-m-some="UNE"
/~lose-"RF24-342H13"
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Direct Submission
Submitted (22 SEP 1999) OB/GYN, Yale University, 333 Cedar Street,
New Haven, CT 06511, USA
                                       Homo sapiens
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/cell_line-"Bix3"
/cell_type-"epithelial cancer cells"
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Mismatches:
                                                                           1 (bases 1 to 475)
Chen, Z.C., Fadiel, A. and Naftolin, F.
Ezrin gene mutation in ovarian cancer
Unpublished
2 (bases 1 to 475)
Chen, Z.C., Fadiel, A. and Naftolin, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
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Ab zref-"taxon:9606"
/chromosome-"6"
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Best Local Similarity:
Query Match:
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                                       ORGANISM
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AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                              AUTHORS
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Search completed: January 16, 2003, 19:05:54 Job time : 1034.47 secs

446 GACT-GATGC1GGGG1GTAGGACIA1CAA 475

1 GluLeuMetLeuArgLeuGlnAspTyrGlu 10

US 09-856-070-23 (1 11) x AF188897 (1-475)